



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/758,636  
Source: IFWO  
Date Processed by STIC: 1/29/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/758,636</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use <b>space characters</b> , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220> _____ →	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

4 <110> APPLICANT: Han, Hui-Quan  
 5 Kwak, Keith  
 7 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family  
 9 <130> FILE REFERENCE: 01017/35966C  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/758,636  
 C--> 12 <141> CURRENT FILING DATE: 2003-01-15  
 14 <150> PRIOR APPLICATION NUMBER: US 09/724,126  
 15 <151> PRIOR FILING DATE: 2000-11-28  
 17 <150> PRIOR APPLICATION NUMBER: US 60/187,911  
 18 <151> PRIOR FILING DATE: 1999-03-08  
 20 <160> NUMBER OF SEQ ID NOS: 29  
 22 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

511 <210> SEQ ID NO: 2  
 512 <211> LENGTH: 1749  
 513 <212> TYPE: PRT  
 514 <213> ORGANISM: Homo sapiens  
 516 <400> SEQUENCE: 2  
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 518 1 5 10 15  
 520 Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln  
 521 20 25 30  
 523 Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro  
 524 35 40 45  
 526 Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu  
 527 50 55 60  
 529 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly  
 530 65 70 75 80  
 532 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe  
 533 85 90 95  
 535 Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys  
 536 100 105 110  
 538 Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe  
 539 115 120 125  
 541 Gln Asp Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr  
 542 130 135 140  
 544 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly  
 545 145 150 155 160  
 547 Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala Gly Thr Ile Lys Glu  
 548 165 170 175

Does Not Comply  
 Corrected Diskette Needed

pp 4-6

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Input Set : A:\35966C.txt

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550 Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile Val Gln Ala Arg Lys
551          180          185          190
553 Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu Met Thr Ile Trp Glu
554          195          200          205
556 Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu
557          210          215          220
559 Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His
560 225          230          235          240
562 Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala
563          245          250          255
565 Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys
566          260          265          270
568 Ala Gly Ala Tyr Ala Ala Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser
569          275          280          285
571 His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His
572          290          295          300
574 Ser Glu Ile Met Ala His Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp
575 305          310          315          320
577 Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys
578          325          330          335
580 Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu Asn Pro Cys Leu Ile
581          340          345          350
583 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys
584          355          360          365
586 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr
587          370          375          380
589 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Gln Leu Gln
590 385          390          395          400
592 Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser Ile Ser Ile Thr Ala
593          405          410          415
595 Leu Ser Val Gln Met Phe Thr Val Pro Thr Leu Ala Arg His Leu Ile
596          420          425          430
598 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val
599          435          440          445
601 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr
602          450          455          460
604 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys
605 465          470          475          480
607 Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr Glu Arg Leu Arg Met
608          485          490          495
610 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met
611          500          505          510
613 Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val
614          515          520          525
616 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn
617          530          535          540
619 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Glu Leu Leu
620 545          550          555          560
622 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr

```

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623				565					570					575
625	Ser	Phe	Ile	Ser	Ser	Ser	Lys	Thr	Val	Val	Gln	Ser	Cys	Gly
626				580					585					590
628	Leu	Glu	Thr	Lys	Ser	Tyr	Arg	Val	Ser	Glu	Asp	Leu	Val	Ser
629				595				600					605	
631	Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	Val	Arg	Leu
632		610					615					620		
634	Leu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Val	Ser	Phe	Glu
635	625					630					635			640
637	Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val
638				645						650				655
640	Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser
641				660					665				670	
643	Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu
644			675					680					685	
646	Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Leu	Met
647		690					695					700		
649	Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	Glu	Leu	Ala
650	705					710					715			720
652	Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	Leu	Ile	Lys
653				725						730				735
655	Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile
656			740						745				750	
658	Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Lys	Glu	Glu
659			755					760					765	
661	Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro
662		770					775					780		
664	Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr
665	785					790					795			800
667	Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly
668				805						810				815
670	Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp
671				820					825					830
673	Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala
674			835						840					845
676	Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Glu	Ala
677		850					855					860		
679	Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Val
680	865					870					875			880
682	Leu	Leu	Asn	Cys	Asp	Ile	Met	Met	Tyr	Ile	Leu	Arg	Thr	Val
683				885						890				895
685	Arg	Ala	Ile	Asp	Thr	Asp	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met
686			900						905					910
688	Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys
689			915						920					925
691	Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Thr	Phe	Asp	Phe	Tyr
692		930					935					940		
694	Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ile	Gln	Met	Leu
695	945					950					955			960

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697 Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp Met Ile Thr
698                               965                               970                               975
700 Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg Glu Lys Ser
701                               980                               985                               990
703 Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp
704                               995                               1000                               1005
706 Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu
707                               1010                               1015                               1020
709 Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala Gln Met Ser Ala Leu
E--> 710 (025) 1025                               1030                               1035                               1040
712 Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met Tyr Asp Asn Thr Ser
713                               1045                               1050                               1055
715 Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu Glu Glu Ser Thr Pro
716                               1060                               1065                               1070
718 Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly Pro Lys Arg Gly Pro
719                               1075                               1080                               1085
721 Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys Gln Glu Glu
722                               1090                               1095                               1100
724 Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val Leu Ser Ala Cys Val
E--> 725 (105) 1105                               1110                               1115                               1120
727 Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro Ile Glu Leu
728                               1125                               1130                               1135
730 Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp Pro Asp Leu Ala Tyr
731                               1140                               1145                               1150
733 Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala Val Cys Trp
734                               1155                               1160                               1165
736 Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln Arg Ile His
737                               1170                               1175                               1180
739 Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys Pro Leu Cys
E--> 740 (185) 1185                               1190                               1195                               1200
742 Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu Gln Pro Gln
743                               1205                               1210                               1215
745 Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln Leu Leu Thr Leu
746                               1220                               1225                               1230
748 Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly Tyr Asn Ile
749                               1235                               1240                               1245
751 Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile Phe Phe Asn Gln Gly
752                               1250                               1255                               1260
754 Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile Leu Ser Phe Gly Val
E--> 755 (265) 1265                               1270                               1275                               1280
757 Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys Glu Met Val Ile Leu
758                               1285                               1290                               1295
760 Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val Pro Pro Asp Glu
761                               1300                               1305                               1310
763 Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser Thr Cys Ala Phe Thr
764                               1315                               1320                               1325
766 Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly Lys Pro Leu Phe
767                               1330                               1335                               1340
769 Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu Lys Ala Leu Met Gln

```

When numbering  
the first  
amino acid on a  
line, begin the  
number directly  
under the first  
letter of the  
amino acid

e.g. Ala | S | Ala  
1025 | P |  
          a  
          c

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E--> 770 345          1350          1355          1360
772 Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln Val Leu Ile Gln Lys
773          1365          1370          1375
775 His Leu Val Arg Leu Leu Ser Val Val Leu Pro Asn Ile Lys Ser Glu
776          1380          1385          1390
778 Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe His Val Leu Val Gly
779          1395          1400          1405
781 Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp Pro Val Asp Leu
782          1410          1415          1420
784 Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His Leu Tyr Leu Phe His
E--> 785 425          1430          1435          1440
787 Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu Thr Val Asp Thr
788          1445          1450          1455
790 Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser Glu Glu Ala His Ser
791          1460          1465          1470
793 Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr Thr Ser Gly Ser Ile
794          1475          1480          1485
796 Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val Ser Leu Lys Asn Gly
797          1490          1495          1500
799 Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe Phe His Tyr Leu Leu
E--> 800 505          1510          1515          1520
802 Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn Ser Ala Glu Gly Glu
803          1525          1530          1535
805 Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro Thr Asn Leu Phe Leu
806          1540          1545          1550
808 Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro Leu Leu Gln Arg Trp
809          1555          1560          1565
811 Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys Gln Lys Asn Thr Val
812          1570          1575          1580
814 Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile Glu Leu Pro Asp Asp
E--> 815 585          1590          1595          1600
817 Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe Arg Cys Pro Arg Ser
818          1605          1610          1615
820 Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys Leu Phe Cys Gly Ala
821          1620          1625          1630
823 Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu Ile Val Asn Gly Glu
824          1635          1640          1645
826 Glu Val Gly Ala Cys Ile Phe His Ala Leu His Cys Gly Ala Gly Val
827          1650          1655          1660
829 Cys Ile Phe Leu Lys Ile Arg Glu Cys Arg Val Val Leu Val Glu Gly
E--> 830 665          1670          1675          1680
832 Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr Gly
833          1685          1690          1695
835 Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser Arg
836          1700          1705          1710
838 Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile Ile
839          1715          1720          1725
841 Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly Phe
842          1730          1735          1740

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844 Asn Trp Gln Leu Leu  
 E--> 845 745

1338 <210> SEQ ID NO: 4  
 1339 <211> LENGTH: 1755  
 1340 <212> TYPE: PRT  
 1341 <213> ORGANISM: Homo sapiens  
 1343 <400> SEQUENCE: 4

1344 Met Ala Ser Glu Leu Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu  
 1345 1 5 10 15  
 1347 Leu Glu Cys Ser Ala Glu Glu Ile Ala Gly Lys Trp Leu Gln Ala Thr  
 1348 20 25 30  
 1350 Asp Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys  
 1351 35 40 45  
 1353 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu  
 1354 50 55 60  
 1356 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu  
 1357 65 70 75 80  
 1359 Asp Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser  
 1360 85 90 95  
 1362 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys  
 1363 100 105 110  
 1365 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe  
 1366 115 120 125  
 1368 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly  
 1369 130 135 140  
 1371 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly  
 1372 145 150 155 160  
 1374 Pro Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu  
 1375 165 170 175  
 1377 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr  
 1378 180 185 190  
 1380 Asn Ile Phe Ala Ile Thr Phe Arg Tyr Ala Val Glu Ile Leu Thr Trp  
 1381 195 200 205  
 1383 Glu Lys Glu Ser Glu Leu Pro Ala Asp Leu Glu Met Val Glu Lys Ser  
 1384 210 215 220  
 1386 Asp Thr Tyr Tyr Cys Met Leu Phe Asn Asp Glu Val His Thr Tyr Glu  
 1387 225 230 235 240  
 1389 Gln Val Ile Tyr Thr Leu Gln Lys Ala Val Asn Cys Thr Gln Lys Glu  
 1390 245 250 255  
 1392 Ala Ile Gly Phe Ala Thr Thr Val Asp Arg Asp Gly Arg Arg Ser Val  
 1393 260 265 270  
 1395 Arg Tyr Gly Asp Phe Gln Tyr Cys Glu Gln Ala Lys Ser Val Ile Val  
 1396 275 280 285  
 1398 Arg Asn Thr Ser Arg Gln Thr Lys Pro Leu Lys Val Gln Val Met His  
 1399 290 295 300  
 1401 Ser Ser Ile Val Ala His Gln Asn Phe Gly Leu Lys Leu Leu Ser Trp  
 1402 305 310 315 320  
 1404 Leu Gly Ser Ile Ile Gly Tyr Ser Asp Gly Leu Arg Arg Ile Leu Cys  
 1405 325 330 335

8-10



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1407 Gln Val Gly Leu Gln Glu Gly Pro Asp Gly Glu Asn Ser Ser Leu Val
1408          340          345          350
1410 Asp Arg Leu Met Leu Ser Asp Ser Lys Leu Trp Lys Gly Ala Arg Ser
1411          355          360          365
1413 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr
1414          370          375          380
1416 Lys Lys Leu Phe Ala Val Arg Phe Ala Lys Asn Tyr Gln Gln Leu Gln
1417 385          390          395          400
1419 Arg Asp Phe Met Glu Asp Asp His Glu Arg Ala Val Ser Val Thr Ala
1420          405          410          415
1422 Leu Ser Val Gln Phe Phe Thr Ala Pro Thr Leu Ala Arg Met Leu Ile
1423          420          425          430
1425 Thr Glu Glu Asn Leu Met Ser Ile Ile Lys Thr Phe Met Asp His
1426          435          440          445
1428 Leu Arg His Arg Asp Ala Gln Gly Arg Phe Gln Phe Glu Arg Tyr Thr
1429          450          455          460
1431 Ala Leu Gln Ala Phe Lys Phe Arg Arg Val Gln Ser Leu Ile Leu Asp
1432 465          470          475          480
1434 Leu Lys Tyr Val Leu Ile Ser Lys Pro Thr Glu Trp Ser Asp Glu Leu
1435          485          490          495
1437 Arg Gln Lys Phe Leu Glu Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys
1438          500          505          510
1440 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile
1441          515          520          525
1443 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu
1444          530          535          540
1446 Thr His Val Ile Ser Met Met Gln Asp Trp Cys Ala Ser Asp Glu Lys
1447 545          550          555          560
1449 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Met Gln Cys
1450          565          570          575
1452 His Gly Gly Tyr Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys
1453          580          585          590
1455 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val
1456          595          600          605
1458 Ser Ile His Leu Pro Val Ser Arg Leu Leu Ala Gly Leu His Val Leu
1459          610          615          620
1461 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu
1462 625          630          635          640
1464 Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu
1465          645          650          655
1467 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe
1468          660          665          670
1470 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg
1471          675          680          685
1473 Glu Met Phe Asp Lys Asp Val Val Met Leu Gln Thr Gly Val Ser Met
1474          690          695          700
1476 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu
1477 705          710          715          720
1479 Tyr Gln Ile Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

1480          725          730          735
1482 Ile Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu
1483          740          745          750
1485 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Ser Pro Gly
1486          755          760          765
1488 Val Gly Gln Val Asn Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His
1489          770          775          780
1491 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu
1492 785          790          795          800
1494 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ala
1495          805          810          815
1497 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu
1498          820          825          830
1500 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe
1501          835          840          845
1503 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys
1504          850          855          860
1506 Arg Gln Asn Arg Glu Asp Thr Ala Leu Pro Pro Pro Val Leu Pro Pro
1507 865          870          875          880
1509 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val
1510          885          890          895
1512 Met Leu Cys Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His Asn
1513          900          905          910
1515 Gly Tyr Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
1516          915          920          925
1518 Gly Met Ala Leu Gln Glu Glu Lys Gln His Leu Glu Asn Val Thr Glu
1519          930          935          940
1521 Glu His Val Val Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
1522 945          950          955          960
1524 Glu Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
1525          965          970          975
1527 Gln Asn Ala Pro Tyr Leu Glu Val His Lys Asp Met Ile Arg Trp Ile
1528          980          985          990
1530 Leu Lys Thr Phe Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr
1531          995          1000          1005
1533 Ser Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
1534          1010          1015          1020
1536 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
E--> 1537 1025/1025          1030          1035          1040
1539 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
1540          1045          1050          1055
1542 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Ala
1543          1060          1065          1070
1545 Ser Thr Ser Ala Val Leu Asp His Ser Pro Val Ala Ser Asp Met Thr
1546          1075          1080          1085
1548 Leu Thr Ala Leu Gly Pro Thr Gln Thr Gln Val Pro Glu Gln Arg Gln
1549          1090          1095          1100
1551 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Val Glu
E--> 1552 105//05          1110          1115          1120

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

1554 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
1555                      1125                      1130                      1135
1557 Ser Lys Asn Arg Ser Lys Phe Ile Gln Asp Pro Glu Lys Tyr Asp Pro
1558                      1140                      1145                      1150
1560 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Ser Ser Cys
1561                      1155                      1160                      1165
1563 Gly His Ile Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
1564                      1170                      1175                      1180
1566 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
E--> 1567 (185) 1185                      1190                      1195                      1200
1569 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
1570                      1205                      1210                      1215
1572 Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Asn Ile Phe Asn
1573                      1220                      1225                      1230
1575 Asn Arg Leu Asn Phe Ser Asp Gln Pro Asn Leu Thr Gln Trp Ile Arg
1576                      1235                      1240                      1245
1578 Thr Ile Ser Gln Gln Ile Lys Ala Leu Gln Phe Leu Arg Lys Glu Glu
1579                      1250                      1255                      1260
1581 Ser Thr Pro Asn Asn Ala Ser Thr Lys Asn Ser Glu Asn Val Asp Glu
E--> 1582 (265) 1265                      1270                      1275                      1280
1584 Leu Gln Leu Pro Glu Gly Phe Arg Pro Asp Phe Arg Pro Lys Ile Pro
1585                      1285                      1290                      1295
1587 Tyr Ser Glu Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Thr
1588                      1300                      1305                      1310
1590 Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Glu Asp Pro Arg Val
1591                      1315                      1320                      1325
1593 Pro Ile Met Cys Trp Gly Ser Cys Ala Tyr Thr Ile Gln Ser Ile Glu
1594                      1330                      1335                      1340
1596 Arg Ile Leu Ser Asp Glu Asp Lys Pro Leu Phe Gly Pro Leu Pro Cys
E--> 1597 (345) 1345                      1350                      1355                      1360
1599 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
1600                      1365                      1370                      1375
1602 Trp Thr Val Ala Ser Val Ser Val Val Gln Gly His Phe Cys Lys Leu
1603                      1380                      1385                      1390
1605 Phe Ala Ser Leu Val Pro Asn Asp Ser His Glu Glu Leu Pro Cys Ile
1606                      1395                      1400                      1405
1608 Leu Asp Ile Asp Met Phe His Leu Leu Val Gly Leu Val Leu Ala Phe
1609                      1410                      1415                      1420
1611 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ile Ser Leu Gly Thr Gly
E--> 1612 (425) 1425                      1430                      1435                      1440
1614 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Ile Gln Ile
1615                      1445                      1450                      1455
1617 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro
1618                      1460                      1465                      1470
1620 Pro Cys Glu Glu Glu Ser Ala Val Leu Ala Leu Tyr Lys Thr Leu His
1621                      1475                      1480                      1485
1623 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ile Pro Ser Gly Trp His Leu
1624                      1490                      1495                      1500
1626 Trp Arg Ser Val Arg Ala Gly Ile Met Pro Phe Leu Lys Cys Ser Ala

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

E--> 1627 505          1510          1515          1520
1629 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ser Pro Pro Asp Ile Gln
1630          1525          1530          1535
1632 Val Pro Gly Thr Ser His Phe Glu His Leu Cys Ser Tyr Leu Ser Leu
1633          1540          1545          1550
1635 Pro Asn Asn Leu Ile Cys Leu Phe Gln Glu Asn Ser Glu Ile Met Asn
1636          1555          1560          1565
1638 Ser Leu Ile Glu Ser Trp Cys Arg Asn Ser Glu Val Lys Arg Tyr Leu
1639          1570          1575          1580
1641 Glu Gly Glu Arg Asp Ala Ile Arg Tyr Pro Arg Glu Ser Asn Lys Leu
E--> 1642 585          1590          1595          1600
1644 Ile Asn Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn
1645          1605          1610          1615
1647 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu
1648          1620          1625          1630
1650 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln
1651          1635          1640          1645
1653 Thr Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr
1654          1650          1655          1660
1656 Ser Cys Gly Ser Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln
E--> 1657 665          1670          1675          1680
1659 Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro
1660          1685          1690          1695
1662 Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn
1663          1700          1705          1710
1665 Pro Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp
1666          1715          1720          1725
1668 His Gln His Ser Val Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
1669          1730          1735          1740
1671 Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
E--> 1672 745          1750          1755
2157 <210> SEQ ID NO: 6
2158 <211> LENGTH: 1755
2159 <212> TYPE: PRT
2160 <213> ORGANISM: Mouse
2162 <400> SEQUENCE: 6
2163 Met Ala Ser Glu Met Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu
2164 1 5 10 15
2166 Leu Glu Cys Ser Ala Glu Glu Ile Ala Gly Arg Trp Leu Gln Ala Thr
2167 20 25 30
2169 Asp Leu Asn Arg Glu Val Tyr Gln His Leu Ala His Cys Val Pro Lys
2170 35 40 45
2172 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Thr Leu
2173 50 55 60
2175 Ala Gln His Ile Leu Leu Gly Pro Met Glu Trp Tyr Ile Cys Ala Glu
2176 65 70 75 80
2178 Asp Pro Ala Leu Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
2179 85 90 95
2181 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys

```

*pp 13-15*

## RAW SEQUENCE LISTING

DATE: 01/27/2004

PATENT APPLICATION: US/10/758,636

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

2182		100		105		110											
2184	Arg	Asp	Cys	Ala	Val	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Glu	Cys	Phe	
2185			115					120					125				
2187	Leu	Gly	Ser	Ile	His	Arg	Asp	His	Arg	Tyr	Arg	Met	Thr	Thr	Ser	Gly	
2188		130					135					140					
2190	Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Glu	Gly	
2191	145					150					155				160		
2193	Pro	Tyr	Cys	Gln	Lys	His	Lys	Leu	Ser	Ser	Ser	Glu	Val	Val	Glu	Glu	
2194				165						170					175		
2196	Glu	Asp	Pro	Leu	Val	His	Leu	Ser	Glu	Asp	Val	Ile	Ala	Arg	Thr	Tyr	
2197			180						185					190			
2199	Asn	Ile	Phe	Ala	Ile	Met	Phe	Arg	Tyr	Ala	Val	Asp	Ile	Leu	Thr	Trp	
2200			195					200					205				
2202	Glu	Lys	Glu	Ser	Glu	Leu	Pro	Glu	Asp	Leu	Glu	Val	Ala	Glu	Lys	Ser	
2203		210					215					220					
2205	Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu	
2206	225				230						235				240		
2208	Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu	
2209				245						250					255		
2211	Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Pro	Val	
2212			260						265					270			
2214	Arg	Tyr	Gly	Asp	Phe	Gln	Tyr	Cys	Asp	Gln	Ala	Lys	Thr	Val	Ile	Val	
2215		275						280					285				
2217	Arg	Asn	Thr	Ser	Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His	
2218		290					295					300					
2220	Ser	Ser	Val	Ala	Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Ala	Leu	Ser	Trp	
2221	305				310						315				320		
2223	Leu	Gly	Ser	Val	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys	
2224				325						330					335		
2226	Gln	Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val	
2227			340						345					350			
2229	Asp	Arg	Leu	Met	Leu	Asn	Asp	Ser	Lys	Leu	Trp	Lys	Gly	Ala	Arg	Ser	
2230			355					360					365				
2232	Val	Tyr	His	Gln	Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr	
2233		370					375					380					
2235	Lys	Lys	Leu	Phe	Ala	Leu	Arg	Phe	Ala	Lys	Asn	Tyr	Arg	Gln	Leu	Gln	
2236	385				390						395				400		
2238	Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala	
2239				405						410					415		
2241	Leu	Ser	Val	Gln	Phe	Phe	Thr	Ala	Pro	Thr	Leu	Ala	Arg	Met	Leu	Leu	
2242			420						425					430			
2244	Thr	Glu	Glu	Asn	Leu	Met	Thr	Val	Ile	Ile	Lys	Ala	Phe	Met	Asp	His	
2245			435					440					445				
2247	Leu	Lys	His	Arg	Asp	Ala	Gln	Gly	Arg	Phe	Gln	Phe	Glu	Arg	Tyr	Thr	
2248		450					455					460					
2250	Ala	Leu	Gln	Ala	Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp	
2251	465					470					475				480		
2253	Leu	Lys	Tyr	Val	Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu	
2254				485						490					495		

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

2256 Arg Gln Lys Phe Leu Gln Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys
2257          500          505          510
2259 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile
2260          515          520          525
2262 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu
2263          530          535          540
2265 Thr His Val Ile Ser Met Val Gln Asp Trp Cys Ala Leu Asp Glu Lys
2266 545          550          555          560
2268 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Thr Gln Cys
2269          565          570          575
2271 His Gly Gly Phe Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys
2272          580          585          590
2274 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val
2275          595          600          605
2277 Ser Ile His Leu Pro Ile Ser Arg Leu Leu Ala Gly Leu His Val Leu
2278 610          615          620
2280 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu
2281 625          630          635          640
2283 Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu
2284          645          650          655
2286 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe
2287          660          665          670
2289 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg
2290          675          680          685
2292 Glu Met Phe Asp Lys Asp Ile Val Met Leu Gln Thr Gly Val Ser Met
2293 690          695          700
2295 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu
2296 705          710          715          720
2298 Tyr Gln Leu Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu
2299          725          730          735
2301 Val Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu
2302          740          745          750
2304 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Asn Pro Gly
2305          755          760          765
2307 Val Gly Gln Val Ala Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His
2308 770          775          780
2310 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu
2311 785          790          795          800
2313 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ser
2314          805          810          815
2316 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu
2317          820          825          830
2319 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe
2320          835          840          845
2322 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys
2323 850          855          860
2325 Arg Glu Asn Lys Glu Asp Thr Ala Leu Pro Pro Pro Ala Leu Pro Pro
2326 865          870          875          880
2328 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Cys Asp Val

```

## RAW SEQUENCE LISTING

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```

2329          885          890          895
2331 Met Leu Tyr Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His His
2332          900          905          910
2334 Gly Ser Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
2335          915          920          925
2337 Gly Met Ala Leu Gln Glu Glu Lys His His Leu Glu Asn Ala Val Glu
2338          930          935          940
2340 Gly His Val Gln Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
2341 945          950          955          960
2343 Asp Ala Pro His Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
2344          965          970          975
2346 Gln Asn Ala Pro Ser Leu Glu Ala His Lys Asp Met Ile Arg Trp Leu
2347          980          985          990
2349 Leu Lys Met Phe Asn Ala Ile Lys Lys Ile Arg Glu Cys Ser Ser Ser
2350          995          1000          1005
2352 Ser Pro Val Ala Glu Ala Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
2353 1010          1015          1020
2355 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
E--> 2356 025/025          1030          1035          1040
2358 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
2359          1045          1050          1055
2361 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Thr
2362          1060          1065          1070
2364 Ser Ala Ser Ala Thr Leu Asp Ser Ser Pro Pro Val Ser Asp Ala Ala
2365 1075          1080          1085
2367 Leu Thr Ala Leu Gly Pro Ala Gln Thr Gln Val Pro Glu Pro Arg Gln
2368 1090          1095          1100
2370 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Thr Val Gly
E--> 2371 105          1110          1115          1120
2373 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
2374          1125          1130          1135
2376 Ser Lys Asp Arg Thr Lys Thr Ile Ala Asp Pro Glu Lys Tyr Asp Pro
2377          1140          1145          1150
2379 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Gly Ser Cys
2380          1155          1160          1165
2382 Gly His Val Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
2383 1170          1175          1180
2385 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
E--> 2386 185          1190          1195          1200
2388 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
2389          1205          1210          1215
2391 Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Ser Ile Leu Ser
2392          1220          1225          1230
2394 Arg Arg Leu Asn Phe Ser Asp Gln Pro Asp Leu Ala Gln Trp Thr Arg
2395          1235          1240          1245
2397 Ala Val Thr Gln Gln Ile Lys Val Val Gln Met Leu Arg Arg Lys His
2398 1250          1255          1260
2400 Asn Ala Ala Asp Thr Ser Ser Ser Glu Asp Thr Glu Ala Met Asn Ile
E--> 2401 265          1270          1275          1280

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

2403 Ile Pro Ile Pro Glu Gly Phe Arg Pro Asp Phe Tyr Pro Arg Asn Pro
2404                               1285                1290                1295
2406 Tyr Ser Asp Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Ala
2407                               1300                1305                1310
2409 Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Gly Asp Pro Arg Val
2410                               1315                1320                1325
2412 Pro Ile Leu Cys Trp Gly Thr Cys Ala Tyr Thr Ile Gln Ser Ile Glu
2413       1330                               1335                1340
2415 Arg Ile Leu Ser Asp Glu Lys Pro Val Phe Gly Pro Leu Pro Cys
E--> 2416 345 1350 1355 1360
2418 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
2419                               1365                1370                1375
2421 Trp Thr Val Ala Leu Leu Pro Val Val Gln Gly His Phe Cys Lys Leu
2422       1380                               1385                1390
2424 Phe Ala Ser Leu Val Pro Ser Asp Ser Tyr Glu Asp Leu Pro Cys Ile
2425       1395                               1400                1405
2427 Leu Asp Ile Asp Met Phe His Leu Leu Val Gly Leu Val Leu Ala Phe
2428       1410                               1415                1420
2430 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ser Ser Leu Ala Thr Gly
E--> 2431 425 1430 1435 1440
2433 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Val Gln Ile
2434       1445                               1450                1455
2436 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro
2437       1460                               1465                1470
2439 Thr Gly Glu Glu Leu Ala Ile Leu Ser Leu His Lys Thr Leu His
2440       1475                               1480                1485
2442 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ala Pro Ser Gly Trp His Leu
2443       1490                               1495                1500
2445 Trp Arg Ser Val Arg Ala Ala Ile Met Pro Phe Leu Lys Cys Ser Ala
E--> 2446 505 1510 1515 1520
2448 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ala Pro Pro Asp Leu Gln
2449       1525                               1530                1535
2451 Val Ser Gly Thr Ser His Phe Glu His Leu Cys Asn Tyr Leu Ser Leu
2452       1540                               1545                1550
2454 Pro Thr Asn Leu Ile His Leu Phe Gln Glu Asn Ser Asp Ile Met Asn
2455       1555                               1560                1565
2457 Ser Leu Ile Glu Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu
2458       1570                               1575                1580
2460 Asn Gly Glu Arg Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu
E--> 2461 585 1590 1595 1600
2463 Ile Asp Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn
2464       1605                               1610                1615
2466 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu
2467       1620                               1625                1630
2469 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln
2470       1635                               1640                1645
2472 Ala Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr
2473       1650                               1655                1660
2475 Ser Cys Gly Ser Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln

```



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

E--> 2476 665 1670 1675 1680  
 2478 Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro  
 2479 1685 1690 1695  
 2481 Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn  
 2482 1700 1705 1710  
 2484 Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp  
 2485 1715 1720 1725  
 2487 Gln Gln His Ser Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn  
 2488 1730 1735 1740  
 2490 Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu  
 E--> 2491 745 1750 1755  
 2955 <210> SEQ ID NO: 18  
 2956 <211> LENGTH: 5205  
 2957 <212> TYPE: DNA  
 2958 <213> ORGANISM: Homo sapiens  
 2960 <400> SEQUENCE: 18  
 2961 atggcggacg aggaggctgg aggtactgag aggatggaaa tcagcgcgga gttaccccag 60  
 2963 acccctcagc gtctggcatc ttggtgggat cagcaagttg atttttatac tgctttcttg 120  
 2965 catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180  
 2967 aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttatttggg 240  
 2969 gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300  
 2971 agggttttca aaagtggaga gacaacctat tcttgaggg attgtgcaat tgatccaaca 360  
 2973 tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420  
 2975 catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480  
 2977 cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540  
 2979 ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600  
 2981 gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660  
 E--> 2983 knryyvdh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720  
 2985 gccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780  
 2987 tatgtctgct gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840  
 2989 catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg 900  
 2991 cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgactttag gcagatcttt 960  
 2993 tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcagggtta 1020  
 2995 atgctttggg atgcaaagct ttataaaggt gcccgtaaga tccttcatga attgatcttc 1080  
 2997 agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat 1140  
 2999 tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact 1200  
 3001 gcactttcag ttcagatggt tactgttctc actctggctc gacatcttat tgaagagcag 1260  
 3003 aatgttatct ctgtcattac tgaactctg ctagaagttt tacctgagta cttggacagg 1320  
 3005 aacaataaat tcaacttcca gggttatagc caggacaaat tgggaagagt atatgcagta 1380  
 3007 atatgtgacc taaagtatat cctgatcagc aaaccacaa tatggacaga aagattaaga 1440  
 3009 atgcagttcc ttgaaggttt tcgatctttt ttgaagattc ttacctgtat gcagggaatg 1500  
 3011 gaagaaatcc gaagacaggt tgggcaacac attgaagtgg atcctgattg ggaggctgcc 1560  
 3013 attgctatac agatgcaatt gaagaatatt ttactcatgt tccaagagtg gtgtgcttgt 1620  
 3015 gatgaagaac tcttacttgt ggcttataaa gaatgtcaca aagctgtgat gaggtgcagt 1680  
 3017 accagtttca tatctagtag caagacagta gtacaatcgt gtggacatag tttggaaaca 1740  
 3019 aagtcctaca gagtatctga ggatcttgta agcatacatc tgccactctc taggacctt 1800  
 3021 gctgggtcttc atgtacgttt aagcaggctg ggtgctgttt caagactgca tgaatttgtg 1860  
 3023 tcttttgagg actttcaagt agaggacta gtggaatc ctttacgttg tctgggtgtg 1920  
 3025 gttgcccagg ttgttgctga gatgtggcga agaaatggac tgtctcttat tagccagggtg 1980

see  
 p. 22  
 for error  
 explanation

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```
3027 ttttattacc aagatggttaa gtgcagagaa gaaatgtatg ataaagatat catcatgctt 2040
3029 cagattgggtg catctttaat ggatcccaat aagtctctgt tactggtact tcagagggtat 2100
3031 gaacttgccg aggcttttaa caagaccata tctacaaaag accaggattt gattaaacaa 2160
3033 tataatacac taatagaaga aatgcttcag gtccctcatct atattgtggg tgagcggttat 2220
3035 gtacctggag tgggaaatgt gaccaaagaa gaggtcacia tgagagaaat cattcacttg 2280
3037 ctttgcattg aacccatgcc acacagtgcc attgccaaaa atttacctga gaatgaaaat 2340
3039 aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accagggtgta 2400
3041 tcaggccatg gagtttatga actaaaagat gaatcactga aagacttcaa tatgtacttt 2460
3043 tatcattact ccaaaaccca gcatagcaag gctgaacata tgcagaagaa aaggagaaaa 2520
3045 caagaaaaca aagatgaagc attgccgcca ccaccacctc ctgaattctg ccctgctttc 2580
3047 agcaaagtga ttaaccttct caactgtgat atcatgatgt acattctcag gaccgtattt 2640
3049 gagcgggcaa tagacacaga ttctaacttg tggaccgaag ggatgctcca aatggctttt 2700
3051 catattctgg cattgggttt actagaagct aagcaacagc ttcaaaaagc tcctgaagaa 2760
3053 gaagtaacat ttgactttta tcataaggct tcaagattgg gaagttcagc catgaatata 2820
3055 caaatgcttt tggaaaaact caaaggaatt cccagttag aaggccagaa ggacatgata 2880
3057 acgtggatac ttcagatggt tgacacagtg aagcgattaa gagaaaaatc ttgtttaatt 2940
3059 gtagcaacca catcaggatc ggaatctatt aagaatgatg agattactca tgataaagaa 3000
3061 aaagcagaac gaaaaagaaa agctgaagct gctaggctac atcgccagaa gatcatggct 3060
3063 cagatgtctg ccttacagaa aaacttcatt gaaactcata aactcatgta tgacaatata 3120
3065 tcagaaatgc ctgggaaaga agattccatt atggaggaag agagcacccc agcagtcagt 3180
3067 gactactcta gaattgcttt gggctcctaaa cgggggtccat ctgttactga aaaggagggtg 3240
3069 ctgacgtgca tcctttgcc aagaagacag gaggtgaaaa tagaaaaataa tgccatggta 3300
3071 ttatcggcct gtgtccagaa atctactgcc ttaaccacgc acaggggaaa acccatagaa 3360
3073 ctctcaggag aagccctaga cccacttttc atggatccag acttggcata tggaaacttat 3420
3075 acaggaagct gtggctcatgt aatgcacgca gtgtgctggc agaagtattt tgaagctgta 3480
3077 cagctgagct ctgacagcg cattcatgtt gacctttttg acttggaag tggagaatat 3540
3079 ctttgccctc tttgcaaatc tctgtgcaat actgtgatcc ccattattcc tttgcaacct 3600
3081 caaaagataa acagtggaaa tgcagatgct cttgctcaac ttttgacctt ggcacgggtg 3660
3083 atacagactg ttctggccag aatatcaggt tataatataa gacatgctaa aggagaaaaac 3720
3085 ccaattccta ttttctttta tcaaggaatg ggagattcta ctttggagtt ccattccatc 3780
3087 ctgagttttg gcgttgagtc ttcgattaaa tattcaaata gcatcaagga aatggttatt 3840
3089 ctctttgcc caacaattta tagaattgga ttgaaagtgc cacctgatga aagggatcct 3900
3091 cgagtcccca tgetgacctg gagcacctgc gctttcacta tccaggcaat tgaaaaatcta 3960
3093 ttgggagatg aaggaaaacc tctgtttgga gcacttcaaa ataggcagca taatggtctg 4020
3095 aaagcattaa tgcagtttgc agttgcacag aggattacct gtccctcaggt cctgatacag 4080
3097 aaacatctgg ttctgtctct atcagttgtt ctccctaaca taaaatcaga agatacacca 4140
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3101 ttgtattggg atgacctgt tgatctgcag ccttcttcag ttagttcttc ctataaccac 4260
3103 ctttatctct tccatttgat caccatggca cacatgcttc agatactact tacagtagac 4320
3105 acaggcctac cccttgctca ggttcaagaa gacagtgaag aggctcattc cgcattctct 4380
3107 ttctttgcag aaatttctca atatacaagt ggctccattg ggtgtgatat tcctggcttg 4440
3109 tatttgtggg tctcactgaa gaatggcatc accccttctc ttctgtgtgc tgcattgttt 4500
3111 ttccactatt tacttggggt aactccgctt gaggaactgc ataccaattc tgcagaagga 4560
3113 gagtacagtg cactctgtag ctatctatct ttacctaaa atttgttctt gctcttccag 4620
3115 gaatattggg atactgtaag gcccttgctc cagaggcggt gtgcagatcc tgccttacta 4680
3117 aactgtttga agcaaaaaaa caccgtggct aggtacccta gaaaaagaaa tagtttgata 4740
3119 gagcttctct atgactatag ctgcctctct aatcaagctt ctcatttcag gtgcccacgg 4800
3121 tctgcagatg atgagcgaaa gcacctctgc ctctgccttt tctgtggggc tatactatgt 4860
3123 tctcagaaca tttgctgcca ggaaattgtg aacggggaag aggttgagac ttgcattttt 4920
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

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3125 cacgcacttc actgtggagc cggagtctgc attttcctaa aaatcagaga atgccgagtg 4980
3127 gtcctgggtg aaggtaaagc cagaggctgt gcctatccag ctccttactt ggatgaatat 5040
3129 ggagaaacag accctggcct gaagaggggc aacccccctc atttatctcg tgagcggtat 5100
3131 cggaagctcc atttggctcg gcaacaacac tgcattatag aagagattgc taggagccaa 5160
3133 gagactaatc agatgttatt tggattcaac tggcagttac tgtga 5205
3136 <210> SEQ ID NO: 19
3137 <211> LENGTH: 1735 1734 (p.21)
3138 <212> TYPE: PRT
3139 <213> ORGANISM: Homo sapiens
3141 <400> SEQUENCE: 19
3142 Ala Met Glu Gly Asn Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg
3143 1 5 10 15
3145 Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser
3146 20 25 30
3148 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu
3149 35 40 45
3151 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu
3152 50 55 60
3154 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu
3155 65 70 75 80
3157 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys
3158 85 90 95
3160 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu
3161 100 105 110
3163 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu
3164 115 120 125
3166 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys
3167 130 135 140
3169 Met His Thr Ser Thr Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu
3170 145 150 155 160
3172 Ala Trp Lys Thr Gly Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala
3173 165 170 175
3175 Gly Thr Ile Lys Glu Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile
3176 180 185 190
3178 Val Gln Ala Arg Lys Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu
3179 195 200 205
3181 Met Thr Ile Trp Glu Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile
3182 210 215 220
3184 Arg Glu Lys Asn Glu Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His
3185 225 230 235 240
3187 His Ser Tyr Asp His Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys
3188 245 250 255
3190 Glu Leu Ala Glu Ala Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly
3191 260 265 270
3193 Arg Arg Ala Val Lys Ala Gly Ala Tyr Ala Ala Cys Gln Glu Ala Lys
3194 275 280 285
3196 Glu Asp Ile Lys Ser His Ser Glu Asn Val Ser Gln His Pro Leu His
3197 290 295 300
3199 Val Glu Val Leu His Ser Glu Ile Met Ala His Gln Lys Phe Ala Leu

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

3200 305          310          315          320
3202 Arg Leu Gly Ser Trp Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe
3203          325          330          335
3205 Arg Gln Ile Phe Cys Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu
3206          340          345          350
3208 Asn Pro Cys Leu Ile Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr
3209          355          360          365
3211 Lys Gly Ala Arg Lys Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe
3212          370          375          380
3214 Met Glu Met Glu Tyr Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr
3215 385          390          395          400
3217 Tyr Lys Gln Leu Gln Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser
3218          405          410          415
3220 Ile Ser Ile Thr Ala Leu Ser Val Gln Met Phe Thr Val Pro Thr Leu
3221          420          425          430
3223 Ala Arg His Leu Ile Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu
3224          435          440          445
3226 Thr Leu Leu Glu Val Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe
3227          450          455          460
3229 Asn Phe Gln Gly Tyr Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val
3230 465          470          475          480
3232 Ile Cys Asp Leu Lys Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr
3233          485          490          495
3235 Glu Arg Leu Arg Met Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys
3236          500          505          510
3238 Ile Leu Thr Cys Met Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly
3239          515          520          525
3241 Gln His Ile Glu Val Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln
3242          530          535          540
3244 Met Gln Leu Lys Asn Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys
3245 545          550          555          560
3247 Asp Glu Glu Leu Leu Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val
3248          565          570          575
3250 Met Arg Cys Ser Thr Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln
3251          580          585          590
3253 Ser Cys Gly His Ser Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp
3254          595          600          605
3256 Leu Val Ser Ile His Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His
3257          610          615          620
3259 Val Arg Leu Ser Arg Leu Gly Ala Val Ser Arg Leu His Glu Phe Val
3260 625          630          635          640
3262 Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg
3263          645          650          655
3265 Cys Leu Val Leu Val Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn
3266          660          665          670
3268 Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys
3269          675          680          685
3271 Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala
3272          690          695          700

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

3274 Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr
3275 705 710 715 720
3277 Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp
3278 725 730 735
3280 Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu
3281 740 745 750
3283 Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr
3284 755 760 765
3286 Lys Glu Glu Val Thr Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu
3287 770 775 780
3289 Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn
3290 785 790 795 800
3292 Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys
3293 805 810 815
3295 Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser
3296 820 825 830
3298 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His
3299 835 840 845
3301 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys
3302 850 855 860
3304 Asp Glu Ala Leu Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe
3305 865 870 875 880
3307 Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu
3308 885 890 895
3310 Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr
3311 900 905 910
3313 Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu
3314 915 920 925
3316 Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe
3317 930 935 940
3319 Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile
3320 945 950 955 960
3322 Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln
3323 965 970 975
3325 Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg
3326 980 985 990
3328 Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu
3329 995 1000 1005
3331 Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg
3332 1010 1015 1020
3334 Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
3335 1025 1030 1035 1040
3337 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met
3338 1045 1050 1055
3340 Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu
3341 1060 1065 1070
3343 Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly
3344 1075 1080 1085
3346 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

3347      1090      1095      1100
3349 Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val
3350 1105      1110      1115      1120
3352 Leu Ser Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly
3353      1125      1130      1135
3355 Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp
3356      1140      1145      1150
3358 Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met
3359      1155      1160      1165
3361 His Ala Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser
3362      1170      1175      1180
3364 Gln Gln Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr
3365 1185      1190      1195      1200
3367 Leu Cys Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile
3368      1205      1210      1215
3370 Pro Leu Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala
3371      1220      1225      1230
3373 Gln Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile
3374      1235      1240      1245
3376 Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile
3377      1250      1255      1260
3379 Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile
3380 1265      1270      1275      1280
3382 Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys
3383      1285      1290      1295
3385 Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys
3386      1300      1305      1310
3388 Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser
3389      1315      1320      1325
3391 Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu
3392      1330      1335      1340
3394 Gly Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu
3395 1345      1350      1355      1360
3397 Lys Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln
3398      1365      1370      1375
3400 Val Leu Ile Gln Lys His Leu Val Arg Leu Leu Ser Val Val Leu Pro
3401      1380      1385      1390
3403 Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe
3404      1395      1400      1405
3406 His Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp
3407      1410      1415      1420
3409 Asp Pro Val Asp Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His
3410 1425      1430      1435      1440
3412 Leu Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu
3413      1445      1450      1455
3415 Leu Thr Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser
3416      1460      1465      1470
3418 Glu Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr
3419      1475      1480      1485

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:30

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

```

3421 Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val
3422      1490      1495      1500
3424 Ser Leu Lys Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe
3425 1505      1510      1515      1520
3427 Phe His Tyr Leu Leu Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn
3428      1525      1530      1535
3430 Ser Ala Glu Gly Glu Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro
3431      1540      1545      1550
3433 Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro
3434      1555      1560      1565
3436 Leu Leu Gln Arg Arg Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys
3437 1570      1575      1580
3439 Gln Lys Asn Thr Val Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile
3440 1585      1590      1595      1600
3442 Glu Leu Pro Asp Asp Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe
3443      1605      1610      1615
3445 Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys
3446      1620      1625      1630
3448 Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu
3449      1635      1640      1645
3451 Ile Val Asn Gly Glu Glu Val Gly Ala Cys Ile Phe His Ala Leu His
3452 1650      1655      1660
3454 Cys Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr
3455 1665      1670      1675      1680
3457 Gly Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser
3458      1685      1690      1695
3460 Arg Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile
3461      1700      1705      1710
3463 Ile Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly
3464      1715      1720      1725
E--> 3466 Phe Asn Trp Gln Leu Leu*
E--> 3467      1730

```

1735 delete

DO NOT include ending stop codon.

see p. 23 for more errors

VARIABLE LOCATION SUMMARY

DATE: 01/27/2004

PATENT APPLICATION: US/10/758,636

TIME: 10:59:31

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

*err explanation*  
Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:18; N Pos. 662,668



10/758,636

23

<210> 16

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 16

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

insufficient explanation.

Give source of genetic material.

(see item 11 on Enr summary sheet)

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/758,636

DATE: 01/27/2004

TIME: 10:59:31

Input Set : A:\35966C.txt

Output Set: N:\CRF4\01272004\J758636.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:710 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:1537 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
M:332 Repeated in SeqNo=4  
L:2356 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6  
M:332 Repeated in SeqNo=6  
L:2983 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18  
L:3466 M:342 E: Invalid Stop Code On Error, STOP CODON:\*  
L:3467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19